

US Ser. No. 09/673,779 -3-
Marked-up Copy of Amended Claims
January 31, 2003

WHAT IS CLAIMED IS:

1. (Amended) A method for identifying the presence of a bacterium in a sample comprising
 - a) testing said sample by Gram-staining and
 - b) testing said sample with a probe according to an *in situ* hybridisation protocol selected on the basis of the outcome of said Gram-staining; and identifying the presence of the bacterium in the sample.
2. A method according to claim 1 wherein said sample is a clinical sample.
3. (Amended) A method according to claim 2 wherein said sample is mammalian blood, ~~preferably being derived from a human.~~
4. (Twice Amended) A method according to claim 1 ~~wherein~~when said Gram-staining indicates the presence of a Gram-negative bacterium in said sample, further comprising determining the rod or coccus character of said bacterium.
5. (Amended) A method according to claim 4 wherein said character is of the rod type, further comprising hybridising said sample with at least one probe selected from a group consisting of probes capable of hybridising with nucleic acid found *Escherichia coli*, in *Klebsiella pneumoniae*, in *Klebsiella oxytoca*, in *Serratia marcescens*, in *Enterobacter aerogenes*, in *Enterobacter cloacae*, in *Proteus vulgaris*, in *Proteus mirabilis*, in *Salmonella typhi*, in *Pseudomonas aeruginosa*.
6. A method according to claim 5 wherein said nucleic acid is ribosomal RNA.
7. (Twice Amended) A method according to claim 5 wherein said probe is selected from a group consisting of probes capable of hybridising with nucleic acid found in more than five, ~~preferably no more than two~~ mismatches with a probe selected of a group

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~~composed~~ consisting of probes having a sequence GCCTGCCAGTTTCGAATG (SEQ ID NO:1) or GTAGCCCTACTCGTAAGG (SEQ ID NO:2) or GAGCAAAGGTATTAACCTTACTCCC (SEQ ID NO:3) or GTTAGCCGTCCTTTCTGG (SEQ ID NO:4).

8. A method according to claim 4 wherein said character is of the coccus type, further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme.

9. (Twice Amended) A method according to claim 1, ~~wherein~~ when said Gram-staining indicates the presence of a Gram-positive bacterium in said sample, further comprising determining the rod or coccus character of said bacterium.

10. A method according to claim 9 wherein said character is of the rod type, further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme and/or Proteinase K.

11. (Amended) ~~A~~ a method according to claim 9 wherein said character is of the coccus type, further comprising determining a chain-like or clump-like character of said bacteria.

12. A method according to claim 11 wherein said character is chain-like, further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme.

13. (Amended) A method according to claim 12 further comprising hybridising said sample with at least one probe selected from a group consisting of probes capable of hybridising with nucleic acid found in *Enterococcus faecalis*, in *Streptococcus pneumoniae*,

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14. A method according to claim 13 wherein said nucleic acid is ribosomal RNA.

15. (Twice Amended) A method according to claim 14 wherein said probe is having no more than five, ~~preferably no more than two~~ mismatches with a probe selected of a group composed of probes having a sequence TTATCCCCCTCTGATGGG (SEQ ID NO:5) or AGAGAAGCAAGCTTCTCGTCCG (SEQ ID NO:10) or GCCACTCCTCTTTTCCGG (SEQ ID NO:7).

16. A method according to claim 11 wherein said character is clump-like, further comprising subjecting said sample to treatment with a lysis buffer comprising lysostaphin and/or Proteinase K.

17. (Amended) A method according to claim 16 further comprising hybridising said sample with at least one probe selected from a group consisting of probes capable of hybridising with nucleic acid found in *Staphylococcus aureus*, in *Staphylococcus haemolyticus*, in *Staphylococcus saprophyticus*.

18. A method according to claim 17 wherein said nucleic acid is ribosomal RNA.

19. (Twice Amended) A method according to claim 18 wherein said probe is having no more than five, ~~preferably no more than two~~ mismatches with a probe selected of a group ~~composed~~ consisting of probes having a sequence GCTAATGCAGCGCGGATCC (SEQ ID NO:8) or CCGAAGGGGAAGGCTCTA (SEQ ID NO:9) or AGAGAAGCAAGCTTCTCGTCCGTT (SEQ ID NO:10).

negative control probe.

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21. (Amended) A method according to claim 20 wherein said positive control probe comprising no more than five mismatches with a probe with the sequence GCTGCCTCCCGTAGGAGT (SEQ ID NO:11) and/or wherein said negative control probe comprises no more than five mismatches with a probe with the sequence ACTCCTACGGGAGGCAGC (SEQ ID NO:12).

22. (Twice Amended) A method according to ~~anyone of~~ claim 1 further comprising a one-step procedure to ~~bind~~of binding bacteria present in said sample to a microscopic slide and simultaneously fixing intracellular structures.

23. (Twice Amended) A method according to ~~anyone of~~ claim 1 wherein said probe is selected for its properties of reactivity with a selected one or a group~~more~~ of bacterial genera and/or species having congruent including a consideration of the susceptibility to antibiotic treatment of said probe.